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ADAMTS-E nucleotide sequence [SEQ ID NO: 1]

CACGCGTCCGACGCGCGGGGGGCCCCGGGCGCGCGCGGGGGCCCGGTGAT GCTGCGAAGGCTGTGAACAGGGGAGGCGGCACTGTGGGGGCTGCCGGCAGCCGGG CTGGGGAGAGACATGTGGACACGTGGCCTCTATGGCTCCCGCCTGCCAGATCCTCCGC AAGATGAGTTCCTGTCCAGTCTGGAGAGCTATGAGATCGCCTTCCCCACCCGCGTGGAC CACAACGGGGCACTGCTGGCCTTCTCGCCACCTCCTCCCGGAGGCAGCGCCGCGGC ACGGGGCCACAGCCGAGTCCCGCCTCTTCTACAAAGTGGCCTCGCCCAGCACCCACT 10 TCCTGCTGAACCTGACCCGCAGCTCCCGTCTACTGGCAGGGCACGTCTCCGTGGAGTA CTGGACACGGGAGGGCCTGGCCTGGCAGAGGGCGGCCCGGCCCACTGCCTCTACGC TGGTCACCTGCAGGGCCAGGCCAGCACCTCCCATGTGGCCATCAGCACCTGTGGAGGC CTGCACGGCCTGATCGTGGCAGACGAGGAAGAGTACCTGATTGAGCCCCTGCACGGTG GGCCCAAGGGTTCTCGGAGCCCGGAGGAAAGTGGACCACATGTGGTGTACAAGCGTTC 15 CTCTCTGCGTCACCCCACCTGGACACAGCCTGTGGAGTGAGAGATGAGAAACCGTGG AAAGGGCGGCCATGGTGGCTGCGGACCTTGAAGCCACCGCCTGCCAGGCCCCTGGGG AATGAAACAGAGCGTGGCCAGCCAGGCCTGAAGCGATCGGTCAGCCGAGAGCGCTACG TGGAGACCCTGGTGGTGGCTGACAAGATGATGGTGGCCTATCACGGGCGCCGGGATGT GGAGCAGTATGTCCTGGCCATCATGAACATTGTTGCCAAACTTTTCCAGGACTCGAGTCT 20 GGGAAGCACCGTTAACATCCTCGTAACTCGCCTCATCCTGCTCACGGAGGACCAGCCCA CTCTGGAGATCACCCACCATGCCGGGAAGTCCCTGGACAGCTTCTGTAAGTGGCAGAAA TCCATCGTGAACCACAGCGGCCATGGCAATGCCATTCCAGAGAACGGTGTGGCTAACCA TGACACAGCAGTGCTCATCACACGCTATGACATCTGCATCTACAAGAACAAACCCTGCG GCACACTAGGCCTGGCCCCGGTGGGCGGAATGTGTGAGCGCGAGAGAAGCTGCAGCG 25 TCAATGAGGACATTGGCCTGGCCACAGCGTTCACCATTGCCCACGAGATCGGGCACACA TTCGGCATGAACCATGACGGCGTGGGAAACAGCTGTGGGGCCCGTGGTCAGGACCCAG CCAAGCTC ATGGCTGCCCACATTACCATGAAGACCAACCCATTCGTGTGGTCATCCTGC AGCCG FGACTACATCACCAGCTTTCTAGACTCGGGCCTGGGGCTCTGCCTGAACAACCG GCCCCCCAGACAGGACTTTGTGTACCCGACAGTGGCACCGGGCCAAGCCTACGATGCA 30 GATGAGCAATGCCGCTTTCAGCATGGAGTCAAATCGCGTCAGTGTAAATACGGGGAGGT CTGCAGCGAGCTGTGGTGTCTGAGCAAGAGCAACCGGTGCATCACCAACAGCATCCCG GCCGCCGAGGCCACGCTGTGCCAGACGCACACCATCGACAAGGGGTGGTGCTACAAAC GGGTCTGTGTCCCCTTTGGGTCGCGCCCAGAGGGTGTGGACGGAGCCTGGGGGCCGT GGACTCCATGGGGCGACTGCAGCCGGACCTGTGGCGGCGGCGTGTCCTCTTCTAGCC 35

GTGCAGTGTTCTGAATTTGACAGCATCCCTTTCCGTGGGAAATTCTACAAGTGGAAAACG TACCGGGGAGGGGGCGTGAAGGCCTGCTCGCTCACGTGCCTAGCGGAAGGCTTCAACT TCTACACGGAGAGGGCGCAGCCGTGGTGGACGGGACACCCTGCCGTCCAGACACGG TGGACATTTGCGTCAGTGGCGAATGCAAGCACGTGGGCTGCGACCGAGTCCTGGGCTC CGACCTGCGGGAGGACAAGTGCCGAGTGTGTGGCGGTGACGGCAGTGCCTGCGAGAC CATCGAGGGCGTCTTCAGCCCAGCCTCACCTGGGGCCGGGTACGAGGATGTCGTCTGG GCCCTGAAGGGAGACCAGGAGTCCCTGCTGCTGGAGGGGCTGCCCGGGACCCCCCAG CCCCACCGTCTGCCTCTAGCTGGGACCACCTTTCAACTGCGACAGGGGCCAGACCAGG TCCAGAGCCTCGAAGCCCTGGGACCGATTAATGCATCTCTCATCGTCATGGTGCTGGCC CGGACCGAGCTGCCTCCGCTACCGCTTCAATGCCCCCATCGCCCGTGACTCGC TGCCCCCTACTCCTGGCACTATGCGCCCTGGACCAAGTGCTCGGCCCAGTGTGCAGG CGGTAGCCAGGTGCAGGCGGTGGAGTGCCGCAACCAGCTGGACAGCTCCGCGGTCGC CCCCACTACTCCAGTGCCCACAGCAAGCTGCCCAAAAGGCAGCGCGCCTGCAACACG GAGCCTTGCCCTCCAGACTGGGTTGTAGGGAACTGGTCGCTCTGCAGCCGCAGCTGCG ATGCAGGCGTGCGCAGCCGCTCGGTCGTGCCAGCGCCGCGTCTCTGCCGCGGAGG AGAAGGCGCTGGACGACAGCGCATGCCCGCAGCCGCGCCCACCTGTACTGGAGGCCT GCCACGGCCCACTTGCCCTCCGGAGTGGGCGGCCCTCGACTGGTCTGAGTGCACCC CCAGCTGCGGGCCGGGCCTCCGCCACCGCGTGGTCCTTTGCAAGAGCGCAGACCACC GCGCCACGCTGCCCCGGCGCACTGCTCACCCGCCGCCAAGCCACCGGCCACCATGC GCTCTGCACAGTGCGGCGTCGGGCAGCGCAGCGCTCGGTGCGCTGCACCAGCCACA CGGGCCAGGCGTCGCACGAGTGCACGGAGGCCCTGCGGCCGCCGACTACCACGCAGC AGTGTGAGGCCAAGTGCGACAGCCCAACCCCCGGGGACGCCCTGAAGAGTGCAAGG ATGTGAACAAGGTCGCCTACTGCCCCCTGGTGCTCAAATTTCAGTTCTGCAGCCGAGCC GGCCCCGGGGGGGGGGAACTGGGAGGGAAGGGTGAGACGGAGCCGGAAGTTATTT ATTIGGGAACCCCTGCAGGGCCCTGGCTGGGAGGATCCACCCCAACCTCTGCCCCC GCCCCAGGGGCACCCCGACATCCAGGCCACCCCTCATGGTGCTACAGACCCTGCCCT GGGGCCCACACACTCCTGCCAGGAAGCCCTACATCAATAAAGTTCTGTCTTGTGTAGAT TTCTAAAAAAAAAAAAAAA

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FIG 2

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ADAMTS-E amino acid sequence [SEQ ID NO: 2]

MAPACQILRWALALGLGLMFEVTHAFRSQDEFLSSLESYEIAFPTRVDHNGALLAFS PPPPRRORRGTGATAESRLFYKVASPSTHFLLNLTRSSRLLAGHVSVEYWTREGLA WQRAARPHCLYAGHLQGQASTSHVAISTCGGLHGLIVADEEEYLIEPLHGGPKGSR SPEESGPHVVYKRSSLRHPHLDTACGVRDEKPWKGRPWWLRTLKPPPARPLGNE TERGQPGLKRSVSRERYVETLVVADKMMVAYHGRRDVEQYVLAIMNIVAKLFQDSS LGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVNHSGHGNAIPENGVA NHDTAVLITRYDICIYKNKPCGTLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIG HTFGMNHDGVGNSCGARGQDPAKLMAAHITMKTNPFVWSSCSRDYITSFLDSGLG LCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHGVKSRQCKYGEVCSELWCLSK SNRCITNSIPAAEGTLCQTHTIDKGWCYKRVCVPFGSRPEGVDGAWGPWTPWGDC SRTCGGGVSSSSRHCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDFREVQC SEFDSIPFRCKFYKWKTYRGGGVKACSLTCLAEGFNFYTERAAAVVDGTPCRPDTV DICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDV VWIPKGSVHIFIQDLNLSLSHLALKGDQESLLLEGLPGTPQPHRLPLAGTTFQLRQGP DQVQSLEALGPINASLIVMVLARTELPALRYRFNAPIARDSLPPYSWHYAPWTKCSA QCAGGSQVQAVECRNQLDSSAVAPHYCSAHSKLPKRQRACNTEPCPPDWVVGN WSLCSRSCDAGVRSRSVVCQRRVSAAEEKALDDSACPQPRPPVLEACHGPTCPPE WAALDWSECTPSCGPGLRHRVVLCKSADHRATLPPAHCSPAAKPPATMRCNLRRC PPARWVAGEWGECSAQCGVGQRQRSVRCTSHTGQASHECTEALRPPTTTQQCE AKCDSPTPGDGPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCCKTCQGH

Figure 3. Domain structure of ADAMTS-E and translated nucleic acid sequence. A) Diagram of ADAMTS-E showing the following domains and signature motifs (with amino acid numbers in parentheses): prodomain (1-66), furin cleavage site (63-66), metalloproteinase domain (67-453), zinc-binding motif (392-420), disintegrin domain (469-531), TSP1 motif (548-601), and four TSP1-like motifs (829-884, 888-944, 948-1002, and 1007-1058). Overlapping clones covering the indicated sequence segments are depicted at the bottom of the diagram. B) ADAMTS-E nucleotide sequence with translated amino acid sequence above.

 \boldsymbol{A} Disintegrin Domain TSP1-ike Motif Zinc-binding Motif TSP1 Tike Motif Metalloproteinase Domain TSP1-like Motif Funn Cleavage Site (Motif) Prodomain TSP1 Motif TSP1-like Mosf S Clone #10 Cone#11 ADAMTS-E 1104 aa B DACGCGTCCG ACGGCGCGA GGCCCCGGGC GCGCGCAAG AGCCCGGTGA TGCTGCAAAG GCTGTGAACA 33334 5 STRONGARDO TROBERGOOT CORRESCOOR COCCENTED TOROGOCACT ACRACHETT CONTRACTOR TORONTO TOR +: Princesia #1 DACTSTGGGG GCTBCCGGCA GCCGGGGCTG GGGAGAGACA TGTGGACACG TGGCCTCTAT GGCTCCCGCC TGCCA ANNO NO STRACACCC CGAIGGCCGT CGGCCCCGAC CCCTCTCTGT ACACCTGTGC ACCGGAGATA CCGAGGGGGG ACCCTCTA % G L G L M F E V T H 161 TOOGCTGGGC COTESCOOTG GGGCTGGGCC TOATGTTCGA GGTCACGCAC GCCTTCEGGT STOAAGATGA GTT LE TE T P V D H N J A L L A F A F P Prodomain 141 AGTOTOGAGA COTATGAGAT DECOTTODOS ACCOGOGTOG ACCACAACOG GECACTOCTO CONTINTO POR SACIA TOAGACOTOT CGATACTOTA GOGGAAGGGG TGGGGGGACO TGGTGTTGCO COGTGACGAC CGGAAGAGGG GT FF F A S

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<u>GAAADACATG SUCTUTCACC STUCCCOGUT TOSGATUCTA CUTTTACTOU TTACUUGAA AUTOSTADDI TA HITT</u>

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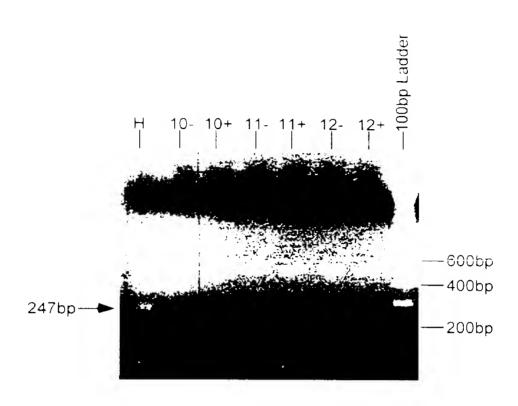


Figure 5. Expression of ADAMTS-E in cDNA from osteoarthritic cartilage.

Figure 6. Amino acid alignment of human ADAMTS-E with a GenSean prediction of ADAMTS-E from mouse genomic sequence.

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r Al AMTB - E		GHGNAIFENGVANHDTAVLITPYDICIYKNKPCGTLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIGHTFGMNHDGV
mACAMT3-E	111	GHGNAIPENGVANHDTAVLITRYDICIYYNKPCGTLGLAPVGGMCERERSCSINEDIGLATAFTIAHEIGHTFGMNHDGV
រុស្សមក្សរភ	4.1	GHGNALFENGVANHETAVLITEYDICIYENFPCGTLGLAPVGGMCEREFSCS NEDIGLATAFTIAHEIGETFGMNHIG.
		981
FATAMTO-E	: 0.0	GNSCGAFGQDPAKLMAAHITMYTNPFVWSSCSRDYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDALEQCPFQ43V
raDAMT3-E	4.5.1	GNGCGAFGQDPAKLMAAHITMFTNFFVWSSCSRDYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDALEQCRFQH3:
ារាស៊ីក្រុងប្រ	4 ÷ 1	GN CGAFGQDPAKLMAAHITMETNEFVWSSCSRDYITSFLDSGLGLCLNNRPPRQDFVYPTVAFGQAYDAIBQOFF.HT
		The second secon
		581
n A C AMT 3 - 8	1.1.	KSRQCYYGEVCSELWCLSKSNFCITNSIPAAEGTLCQTHTIDKGWCYKFVCVPFGSPPEGVDGAWGPWTPWGDCSRTD33
nALAMTS-E	561	ESRQCKYGEVCSELWCLSKSNFCITNSIFAAEGTLCQTHTIDKGWCYKPVCVPFGSPPEGVDGAWGPWTPWGDCSR3CGG
lonsensus	561	ASPACE A CENCER MC SESSION CONTROL OF THE CONTROL OF THE PROPERTY OF THE PROPE
		RSPQCHYGEVOSELWOLSHSNFCITNSIFAAEGTLCQTHTIDKGWCYRPVCVPFGSRPEGVDGAWGPWTFWGDCSP (1)
		641
1.212MT2-E	512	GVSSSSPHCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDFREVQCSEFDSIPFRGKFYKWKTYRGGGVKACSLTDLA
JANAMINE	541	GVSSSSPHCDSPRPTIGGKYCLGEPRRHRSCNTNDCPPGSQDFREMQCSEFDSVPFRGKFYTWKTYRGGGVKACSLTCLA
inthe etcEud	541	GVSSSSBHCDSPRPTIGGKYCLGERRHFSCNT DCPPGSQDFRE QCSEFDS PFRGKFY WKTYPGGGUYAGGLTTLA
		721
MALAMTS-E	692	EGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDVV
~ARAMTS-E	21.	EGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPALPGTGYEEVV
linienss	72:	EGFNFYTERAAAVVDGTPCRPLTVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEG.FSPA PG GYEDVV
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		WIPKGSVHIFIQDLNLSLSHLALKGDQESLLLEGLPGTPQPHRLPLAGTTFHLRQGPDQAQSLEALGPINASLIIMVLA.
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TAUAMITE B	150	TELPALFYRFNAPIARDSLPPYSWHYAPWTYCSAQCAGGSQVQAVECRNQLDSSAVAPHYCSAHSYLPKRQRACNTEPUF
#ALAMTS-E	441	AELPALHYRFNAPIARDALPPYSWHYAPWTKCSAQCAGGSQVQVVECRNQLDSSAVAPHYCSGHSFLPKRQRACNTEPCP
โกกระกรแร	- 5 1	ELPAL YRFNAPIARD LPPYSWHYAPWTKGSAQCAGGSQVQ VECRNQLDSSAVAPHYGS HSKLPKPQPACHTEF 9
		961
	. 7 .	FDWVVGNWSLCSPSCDAGVRSFSVVCORPVSAAEEKALDDSACPOPRPPVLEACHGPTCPPEWAALDWSECTPSCGEGGG
		PDWVGNWSRCSRSCDAGVRSPSVVCORPVSAAEKALDDSACPOPRPPVLEACGGPMCPPEWATLDWSECTPSGFF3LF
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